

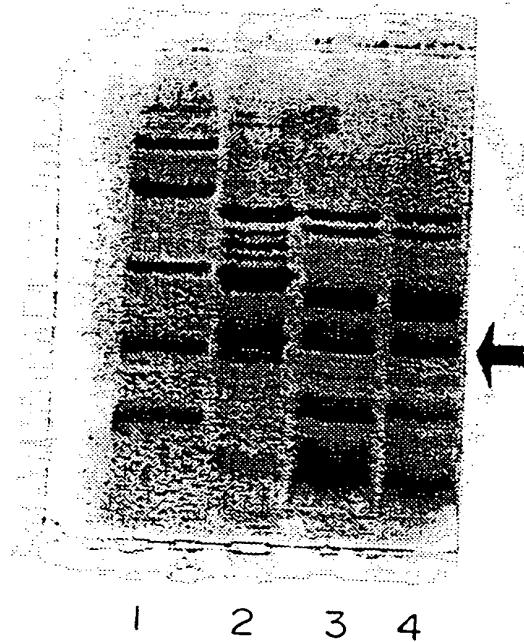
FIGURE 1

5	TOGGCAAAGC AGCCGGATAC CGCTACGTAT CTGAACTAT TGAAAATATT ACGATGCAA AAAGAAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTCTAA CTGACCATAA AGGAACAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC Met Lys Lys Ala Leu Ala Thr Leu Ile Ala -19 -15 -10	60 120 172
10	CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC Leu Ala Leu Pro Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr -5 1 5	220
15	GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Leu Gly Ser 10 15 20	268
20	GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp 25 30 35	316
25	CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro 40 45 50 55	364
30	TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp 60 65 70	412
35	TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser 75 80 85	460
40	CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA Leu Asn Arg Ala Ser Val Asp (Leu) Gly Gly Ser Asp Ser Phe Ser Gln 90 95 100	508
45	ACC TCC ATC CGC CTC GGC GTA TTG AGC GGC GTA AGC TAT GCC GTT ACC Thr Ser (Ile) Gly Leu Gly Val Leu (Thr) Gly Val Ser Tyr Ala Val Thr 105 110 115	556
50	CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys 120 125 130 135	604
55	GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val 140 145 150	652
60	CGC GTC AAA TTC TGATATGGCG CTTATCTGC AAACCGCCGA GCCTTCGGCG Arg Val Lys Phe 155	704
	CTTTTGTTT CTGCCACCGC AACTACACAA GCGGGGGTT TTGTACGATA ATCCCGAATG CTGCGGCTTC TGCGGCCCTA TTTTTGAGG AATCGAAAT GTCCAAAACC ATCATCCACA CCGACA	764 824 830

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FIGURE 2



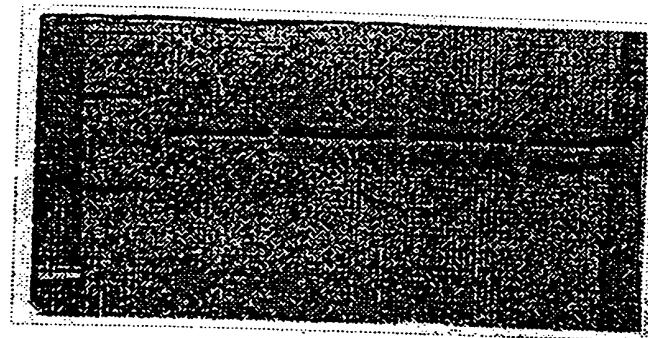
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FIGURE 3a



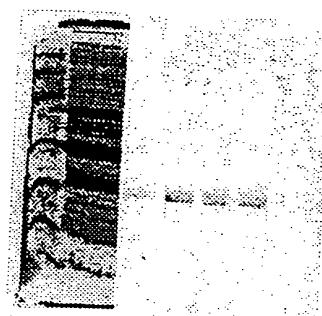
FIGURE 3b



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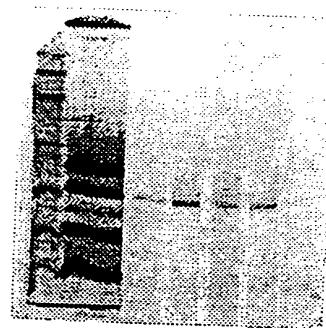
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FIGURE 4a



1 2 3 4 5 6

FIGURE 4b



1 2 3 4 5 6

FIGURE 5

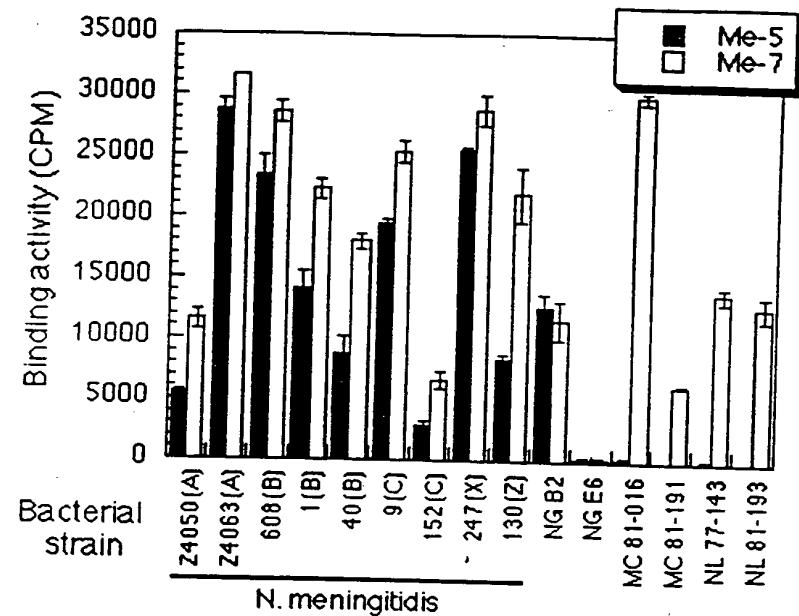
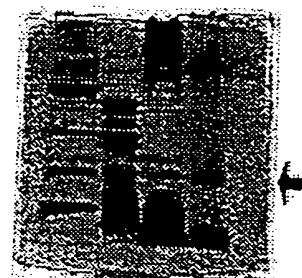


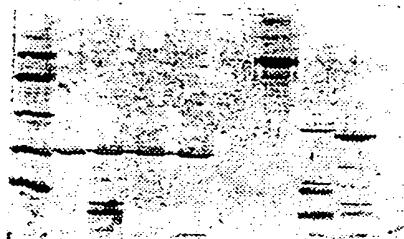
FIGURE 6A



1 2 3 4

02557683 1000000000

FIGURE 6B



1 2 3 4 5 7 8 9 10

FIGURE 6C

NT C T K

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FIGURE 7

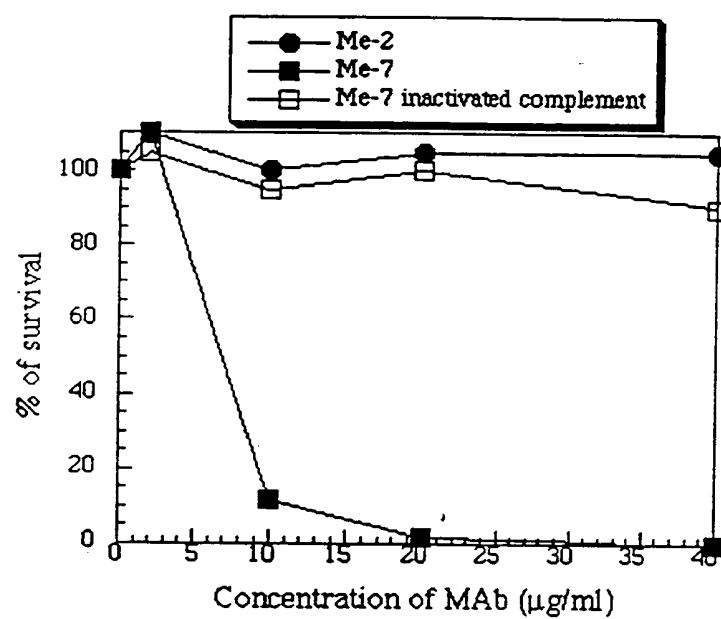


FIGURE 8

5	GTATCTTGAG GCATTGAAAA TATTACAATG CAAAGAAA ATTCAGTAT AATACGGCAG GATTCTTAA CGGATTCTTA ACCATTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG Met -19	60 118
10	AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCC GCC GCA GCA Lys Lys Ala Leu Ala Ala Ile Ala Leu Ala Leu Pro-Ala Ala Ala -15 -10 -5	166
15	CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His 1 5 10	214
20	GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC Ala Lys Ala Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg TAC 15 20 25 30	262
25	ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr 35 40 45	310
30	ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu 50 55 60	358
35	TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro 65 70 75	406
40	GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GGC TCC GTC Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser ,Leu Asn Arg Ala Ser Val 80 85 90	454
45	GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC CGC Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly 95 100 105 110	502
50	GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp 115 120 125	550
55	GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn 130 135 140	598
	GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATAACCC Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe 145 150 155	650
	GTATTTCCGC AAACCGCGGA GCGTTTGGC GGTTTTGTTT TCGGGCGCGG CAACTACACA	710

FIGURE 9

5	CACCCATCGG CGCGGTGATG CGGCCACAC CATTAAAGG CAACGGCGG GTTAACGGCT	60
	TTGGCGTCGG CAAAGCAGCC GGATACCGCT ACGTATCTTG AAGTATTAAA AATATTACGA	120
	TGCAGAAAGA AAATTAAGT ATAATAAACG AGAATTCTTT AACGGATTCT TAACAATTT	180
10	TCTAACTGAC CATAAAGGAA CCAAAAT ATG AAA GCA CTT GCC ACA CTG Met Lys Lys Ala Leu Ala Thr Leu	231
	-19 -15	
15	ATT GCC CTC GCT CTC CCG GCC GCA CTG GCG GAA GGC GCA TCC GCC Ile Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly	279
	-10 -5 1 5	
20	TTT TAC GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu	327
	10 15 20	
25	GGT TCT GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile	375
	25 30 35	
30	AAC GAC CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA Asn Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys	423
	40 45 50	
35	GCC CCA TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile	471
	55 60 65	
40	TAC GAC TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC Tyr Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg	519
	70 75 80 85	
45	TTG AGC CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe	567
	90 95 100	
50	AGC CAA ACC TCC ACC GGC CTC GGC GTA TTG GCG GGC GTA AGC TAT GCC Ser Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala	615
	105 110 115	
55	GTT ACC CCG AAT GTC GAT TTG GAT GGC GGC TAC CGC TAC AAC TAC ATC Val Thr Pro Asn Val Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile	663
	120 125 130	
60	GCC AAA GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GCC Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala	711
	135 140 145	
55	GGT GTG CGC GTC AAA TTC TGATATGGCG CTTATTCTGC AAACCGCCGA Gly Val Arg Val Lys Phe	759
	150 155	
60	GGCTTGGCG GTTTTGTTT CTGCCACCGC AACTACACMA GCGGGGGTT TTGTACGATA ATCCCCGAAATG CTGGGGCTTC TGCGGGCCTTA T	819
		850

FIGURE 10

	CCCCGCCTTT CGGGTTTTT CCAAACCGTT TCCAAGTTTC ACCCATCCGC CGCGTGATGCC	60
5	CGCCGTTAA GGGCAACGCG CGGGTTAACG GATTGCGGT CGGCAGAAGCA GCGGATGCC	120
	GCGCGTATC TTGAGGCATT GAAAATATTA CGATGCAAAA AGAAAATTTTC AGTATAATAC	180
10	GGCAGGATTTC TTAAACGGAT TATTAACAAT TTTCTCCCT GACCATAAAG GAACCAAAAT	240
	ATG AAA AAA GCA CTT GCC GCA CTG ATT GCG CTC GCA CTC CGC GCC CCC Met Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala	288
	-19 -15 -10 -5	
15	GCA CTG GCG GAA GCG GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala	336
	1 5 10	
20	CAC GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro	384
	15 20 25	
25	CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp	432
	30 35 40 45	
30	TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA TCC ACC GAT TTC AAA CTT Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu	480
	50 55 60	
35	TAC AGC ATC GGC GCG TCC GTC ATT TAC GAC TTC GAC ACC CAA TCG CCC Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro	528
	65 70 75	
40	GTC AAA CCG TAT TTC GGC GCG CGC TTG AGC CTC AAC CGC GCT TCC GCC Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala	576
	80 85 90	
45	CAC TTG GGC GGC AGC GAC AGC TTC AGC AAA ACC TCC GCC GGC CTC GGC His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly	624
	95 100 105	
50	GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp	672
	110 115 120 125	
55	GCC GGC TAC CGC TAC AAC TAC GTC GGC AAA GTC AAC ACT GTC AAA AAC Ala Gly Tyr Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn	720
	130 135 140	
	GTC CGT TCC GGC GAA CTG TCC GCC GGC GTG CGC GTC AAA TTC TGATATAACGC Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe	772
	145 150 155	
60	GTTATTCCGC AAACCGCCGA GCCTTGGCG GTTTTTTG	810

FIGURE 11

	MCH88-ORF	G.	C.....	50
5	608B-ORF	A.	T.....	50
	Z4063-ORF	A.	T.....	50
	gono b2-ORF	G.	A.....	50
	Consensus	ATGAAAAAAG	CACTTGCCRC	ACTGATTGCC	CTCGCHCTCC	CGGCCGCGC	CGGCCGCGC	50
10	MCH88-ORF	100
	608B-ORF	100
	Z4063-ORF	100
	gono b2-ORF	100
	Consensus	ACTGGCGGAA	GGCGCATCCG	GCTTTTACGT	CCAAGCCGAT	GCGGCACACG	GCGGCACACG	100
15	MCH88-ORF	.C.....	150
	608B-ORF	.A.....	150
	Z4063-ORF	.A.....	150
	gono b2-ORF	.C.....	150
20	Consensus	CMAAAGCCTC	AAGCTCTTAA	GGTCTTGCCA	AAGGCTTCAG	CCCGGCCATC	CCCGGCCATC	150
	MCH88-ORF	200
	608B-ORF	200
	Z4063-ORF	200
	gono b2-ORF	200
	Consensus	TCCGCAGGCT	ACCGCATCAA	CGACCTCCGC	TTCGCCGTGC	ATTACACGCG	ATTACACGCG	200
	MCH88-ORF	T.....	250
30	608B-ORF	C.....	247
	Z4063-ORF	C.....	247
	gono b2-ORF	C.....	247
	Consensus	CTACAAAAAC	TATAAACAAAG	YCCCATCCAC	CGATTICAAA	CTTTACAGCA	CTTTACAGCA	250
35	MCH88-ORFC.....	300
	608B-ORFC.....	297
	Z4063-ORFC.....	297
	gono b2-ORFT.....	298
	Consensus	TCGGCGCGTC	CGYCATTTCAC	GAATTCGACA	CCCAATCSCC	CGTCAAACCG	CGTCAAACCG	300
40	MCH88-ORF	.C.....C.....T.GTAA..TAA..	350
	608B-ORF	.C.....C.....T.GGGG..GGG..	347
	Z4063-ORF	.C.....C.....T.GGGG..GGG..	347
	gono b2-ORF	.T.....T.....C.CGGG..GGG..	347
	Consensus	TATYTGGCG	CGCGCTTGAG	CCTCAACCGC	GCYTCGGYCS	ACTTKRRCGG	ACTTKRRCGG	350
45	MCH88-ORFC.....	.AC.....G.....G.....	400
	608B-ORFC.....	.AT.....A.....A.....	397
	Z4063-ORFC.....	.AC.....G.....G.....	397
	gono b2-ORFA.....	.GC.....G.....G.....	397
50	Consensus	CAGCGACAGC	TTCAGCMAA	CCTCCRYCGG	CCTCGGGCGTA	TTGRGGGGCG	TTGRGGGGCG	400
	MCH88-ORF	450
	608B-ORF	447
	Z4063-ORF	447
	gono b2-ORF	447
	Consensus	TAAGCTATGC	CGTTACCCCG	AATGTCGATT	TGGATGCCGG	CTACCGCTAC	CTACCGCTAC	450
	MCH88-ORF	A.....T.....	500
60	608B-ORF	A.....C.....	497
	Z4063-ORF	A.....C.....	497
	gono b2-ORF	G.....C.....	497
	Consensus	AACTACRTOG	GCAGAAGTCAA	CACTGTCAAA	AAYGTCGGTT	CCGGCGAACT	CCGGCGAACT	500
65	MCH88-ORFC...CA.....	528
	608B-ORFT...CG.....	525
	Z4063-ORFC...TG.....	525
	gono b2-ORFC...CG.....	525
	Consensus	GTCOOGYCGGY	GTRCGCGTCA	AATTCTGA				528

FIGURE 12

5	gonoB2A.....	50
	Z4063T.....	50
	608BT.....	50
	MCH88A.....	50
	Consensus	MKKALA.LIA	LALPAALAE	GASGFYVQAD	AAHAKASSSL	GSAKGFSPRI	50
10	gonoB2	V..	99
	Z4063	99
	608B	99
	MCH88	QV.....	99
	Consensus	SAGYRINDLR	FAVDYTRYKN	YK-APSTDVK	LYSIGASAIY	DFDTQSPVKP	100	
15	gonoB2	F.....	AH.....	K.A.....	149
	Z4063	T.....	149
	608B	I.....	T.....	149
	MCH88	FN.....	T.....	150
20	Consensus	YLGARLSLNR	ASVDLGGSDS	FSQTS.GLV	LAGVSYAVTP	NVLDAGYRY	150	
	gonoB2	V.....	174
	Z4063	174
	608B	V.	174
25	MCH88	175
	Consensus	NYIGKVNTVK	NVRSGELSAQ	VRVKF	175

FIGURE 13

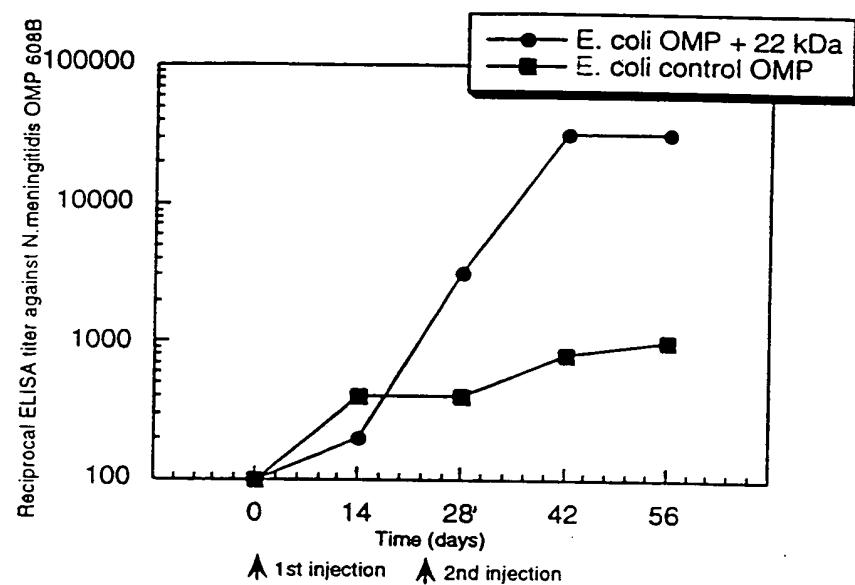


FIGURE 14

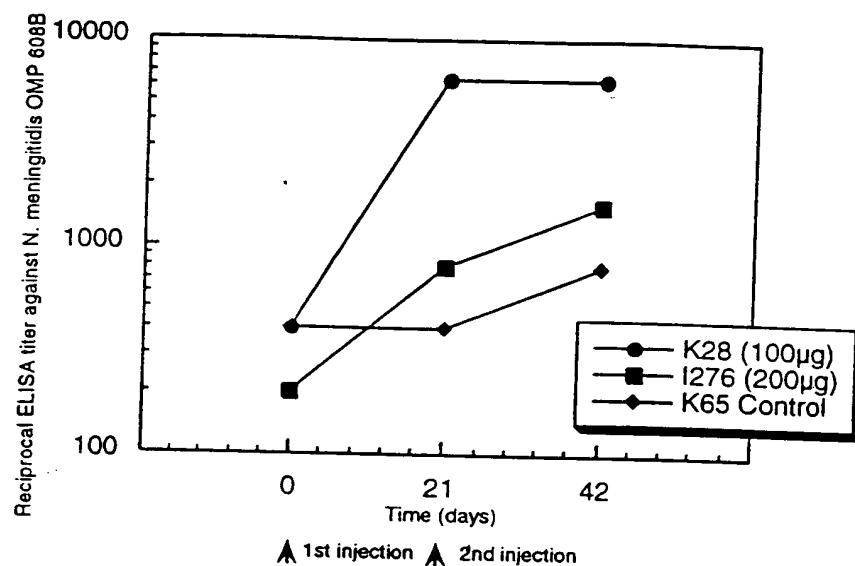


FIGURE 15

	MKKALATLIA	LALPAAALAE	GASGFYVQAD	AAHAKASSL	GSAKGFSPI	50
5	CS-840		CS-842		CS-844	
		CS-841		CS-843		
10	SAGYRINDLR	FAVDYTRYKN	YKAPSTDFKL	YSIGASAIYD	FDTQSPVKPY	100
		CS-846		CS-848		
	CS-845		CS-847		CS-849	
15		CS-857				
	LGARLSLNRA	SVDLGGSDSF	SQTSIGLGVL	TGVSYAVTPN	VDLDAGYRYN	150
20	CS-850		CS-852		CS-854	
		CS-851		CS-853		
25	YIGKVNTVKN	VRSGELSVGV	RVKF			174
		CS-856				
	CS-855					
30						

FIGURE 16

